

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using 'sw model

Run on: April 1, 2003, 08:45:46 ; Search time 47 Seconds
(without alignments)
918.391 Million cell updates/sec

Title: US-09-768-781-3

Perfect score: 2316

Sequence: 1 MDRVVEIPENPNVDPVSSLE.....RTRVENSEPPFTEARQSVV 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	918	39.6	444	2 I39294	McLeod syndrome-as
2	129	5.6	439	2 T32470	hypothetical prote
3	120.5	5.2	382	2 E75203	hypothetical prote
4	119.5	5.2	745	2 T02024	cytochrome b245 be
5	118.5	5.1	783	2 A96825	hypothetical prote
6	113.5	4.9	508	2 D90567	hypothetical prote
7	112.5	4.9	785	2 A86299	hypothetical prote
8	109.5	4.7	461	2 B97305	probable cation ef
9	109.5	4.7	498	2 T11039	NADH2 dehydrogenas
10	108	4.7	459	2 T17163	NADH2 dehydrogenas
11	107	4.6	459	2 T17166	NADH2 dehydrogenas
12	107	4.6	459	2 T17172	NADH2 dehydrogenas
13	106.5	4.6	341	2 G82880	ferric anguibactin
14	105.5	4.6	459	2 T17169	NADH2 dehydrogenas
15	105.5	4.6	1584	2 T00026	brain-specific ang
16	105	4.5	740	2 A06000	probable membrane
17	104.5	4.5	741	2 F90739	probable transport
18	104.5	4.5	741	2 H85589	probable transport
19	104.5	4.5	786	2 H64817	probable membrane
20	103.5	4.5	503	2 D75104	transmembrane tran
21	103.5	4.5	2143	2 G96595	hypothetical prote
22	102.5	4.4	313	2 T25628	hypothetical prote
23	102.5	4.4	378	2 T25628	hypothetical prote
24	102.5	4.4	405	2 S53040	hypothetical prote
25	102.5	4.4	521	2 T15322	probable membrane
26	102.5	4.4	1154	2 T48829	related to SREBP c
27	102	4.4	474	2 S63658	NADH2 dehydrogenas
28	101.5	4.4	438	2 T32208	hypothetical prote
29	101	4.4	459	2 T17181	NADH2 dehydrogenas

30	101	4.4	459	2 T17144	NADH2 dehydrogenas
31	101	4.4	483	2 G84113	hypothetical prote
32	100.5	4.3	264	1 S02157	H+-transporting tw
33	100	4.3	493	2 C86565	oligopeptide perme
34	100	4.3	493	2 D72059	peptide ABC transp
35	100	4.3	570	2 D86304	hypothetical prote
36	100	4.3	599	2 G90476	probable Na+/H+ an
37	99.5	4.3	346	2 T19008	hypothetical prote
38	99.5	4.3	370	2 C69309	conserved hypothet
39	99.5	4.3	575	2 F71360	probable K+ transp
40	99	4.3	423	2 I38056	nicotinic acetylch
41	99	4.3	443	2 C70190	K+ transport prote
42	98.5	4.3	611	2 S61147	TCM10 protein - ye
43	98.5	4.3	1033	2 T39030	probable calcium-t
44	98	4.2	345	2 T26917	hypothetical prote
45	98	4.2	372	2 G83707	hypothetical prote

ALIGNMENTS

RESULT 1

I39294

McLeod syndrome-associated protein XK - human

N;Alternate names: probable membrane transport protein

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 01-Dec-2000

C;Accession: I39294; S69126

R;Ho, M.; Chelly, J.; Carter, N.; Danek, A.; Crocker, P.; Monaco, A.P.

Cell 77, 869-880, 1994

A;Title: Isolation of the gene for McLeod syndrome that encodes a novel membrane transpo

A;Reference number: A54300; MUID:94273191; PMID:8004674

A;Accession: I39294

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-444 <RES>

A;Cross-references: EMBL:732684; NID:9515872; PID:9515873

R;Khamlichi, S.; Bailly, P.; Blanchard, D.; Goossens, D.; Cartron, J.P.; Bertrand, O.

Eur. J. Biochem. 228, 931-934, 1995

A;Title: Purification and partial characterization of the erythrocyte Kx protein defici

A;Reference number: S69126; MUID:95255304; PMID:7737196

A;Accession: S69126

A;Status: preliminary

A;Molecule type: protein

A;Residues: 7-22 <KHA>

C;Genetics:

A;Gene: GDB:XK

A;Cross-references: GDB:120499; OMIM:314850

A;Map position: Xp21.2-Xp21.1

C;Keywords: phosphoprotein; transmembrane protein

Query Match 39.6%; Score 918; DB 2: Length 444;

Best Local Similarity 44.3%; Pred. No. 1.4e-69;

Matches 178; Conservative 80; Mismatches 134; Indels 10; Gaps 4;

QY 33 FPFSEILFELYGEAASALYVRYIKQKSETYRMYTTFSEFFMFSSIMVOLTIFVHRDL 92

Db 3 FPAVSLASVFLFVAETTAALSLSTYRSGGDMQWQALTLFLLPCALVQLTLLFVHRDL 62

QY 93 AKDKPLSLFPHLILLGPVRCLEAMIKYLTWKKEQEEPPYVSLTRKK-MLDGEVLLIE 151

Db 63 SRDRPLVLLHLLQLGLPRCFEVCYI---FQSGNNEEPYVSIITKKRMPQNGLSEIE 119

QY 152 WEVGHISRTLMHNRNAYKMSQIQAFGLGVPLQTYOLYVSLISAIEVPLGRVLMVMSVLS 211

Db 120 KEVQAGEGLIITHRSAFASVSIQAFGLSAPQTLQIYISWMOODVTVGRSLMTILLS 179

QY 212 VTYGATLCNMLAIQIKYDDYKIRGLGPVLCITWRTLEITSLRLILVFSATILKXAVP 271

Db 180 IYVYALRCNMLAIKIKYDYEYKVNPLAYVICFLWRSFEIATRVVVLVLTSLVLTWVV 239

QY 272 FLVLNPLIILFEPWIKFWSGQMPNNIEKFRVGLTVLVLSITVILYAGINFSWALQ 331

Db 240 IILNPFSPFLYDWILFWCSCGSPFENIEKALSRVGTIVLCFLTLTYTGINMFCWSAVQ 299
Qy 332 LRLADRLVDKQNGWGMGLHYSVRLVENVMVLKPKFGVKVLLNYCHSLIALQLIIAY 391
Db 300 LKIDSPLDKSHNWYQOLLVYVYIRFIENAILLLWLFKTDIYMYVCAPELLVLQLLIGY 359
Qy 392 LISIDFMLLFFQYLHLPLSLRSLTHNVVD-----YLHCVC--CHQ 427
Db 360 CTAILLPLVFPYFFHCKKLFSSSVSEGFQWLRCFCWCACRQ 401
RESULT 2
T32470
hypothetical protein F08F1.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
R:Fulton, B.
C:Accession: T32470
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid F08F1.
A:Reference number: Z21174
A:Accession: T32470
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-439 <FUL>
A:Cross-references: EMBL:AF026213; PIDN:AAB71305.1; GSPDB:GN00028; CESP:F08F1.5
A:Experimental source: strain Bristol N2; clone F08F1
C:Genetics:
A:Gene: CESP:F08F1.5
A:Map position: X
A:Introns: 20/1; 72/3; 137/3; 184/2; 263/3; 289/3; 339/3; 369/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F08F1.5
Query Match 5.6%; Score 129; DB 2; Length 439;
Best Local Similarity 19.4%; Pred. No. 0.004;
Matches 67; Conservative 62; Mismatches 98; Indels 118; Gaps 15;
Qy 97 PLSLFWHLIL--LGPVIRCLAMIKYLTWKKEQEPEYVSLTRKMKLIDGEEVLEWV 154
Db 126 PLSRMIVLCIQMGPLFYWKALY-YGMFPRKSNEN-----TDGEX----- 166
Qy 155 GHSIRTLAMHRNAYKMSQ-----IQAFGLSGVPOL----- 184
Db 167 -----RKCFKSNVEARDATLLRFFAEFLASAPQLIIOGSTAASYFQNYQTGY 216
Qy 185 TYQYVSLISAEPVLRVLMVFLSVYTGATLCNNLAIQIKYDDYKIRGLPLEVLCIT 244
Db 217 PYWLYFOAAS-----LLLSIISISWVQNRSLRMIR--DDKVNWPHEAVLQF 264
Qy 245 IWTLEITRLLILVLSATLKLKAVPFLVNLFLIILFEPWIKFWRSGAOMPNNIEKNFS 304
Db 265 CWRFLTLARIITLVA-----LVLI-----GINVAIHIDA-CT 297
Qy 305 RVGLTVLLSVTILYAGINFSCWSALQLRLADRLVDKQNGWGMGLHYSVRLVENVMV 364
Db 298 HIEKLLLLIN-TIHIIFIP-----NMVGNTRWRYL-TAYSVEFIE---MM 399
Qy 365 LVKPFPGVKVLLNYCHSLIALQLIIAYLISIDFMLLFFQYLHLPLR 409
Db 340 LVCWLLPLSLNTPFYIEKVKVGVGPISFIAGIAMMYVQFFHPNR 384
RESULT 3
E75203
hypothetical protein PAB2250 - Pyrococcus abyssi (strain Oresay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: E75203
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: E75203

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <KAW>
A:Cross-references: GB:AJ248283; GB:AL096836; NID:G5457433; PIDN:CAB49076.1; PID:E15149;
A:Experimental source: strain Oresay
C:Genetics:
A:Gene: PAB2250
Query Match 5.2%; Score 120.5; DB 2; Length 382;
Best Local Similarity 22.7%; Pred. No. 0.018;
Matches 83; Conservative 56; Mismatches 151; Indels 75; Gaps 14;
Qy 72 SFEM---FSSIMVQLTLIFVHRDLAKDKPLSLFMHLIILGPIRCLEAMIKYLTWKKEE 128
Db 49 SFILARAFSSLFSGLL-----LEKDK-----RLIYLGSVTMAGNALIVHL----- 88
Qy 129 QEEPYVSLTRKMKLIDGEEVL-----IEWEVGHSIRTLAMHRNAYKMSQIQAFGLGSPV 182
Db 89 -----YPLTTSWIQVVGIKILNGLLNGISWPFAQFAIASASPDNVRARVTSVYFFLASVA 143
Qy 183 QLTQYLYVSLISAEPVLRVLMVFLSVYTGATLCNNLA---IQIKYDDYKIRGLPLE 239
Db 144 SVIGN-YVYAQMAELTLKQMM---VASIFYLLTALSMPFLAYLIFYNYVTPKRKGNVE 198
Qy 240 VLCITWRTLEITSLRLIILVLFSA-----TLKLVKAVPFLVNLFLIIL 281
Db 199 ELHLDPRKVLVITSLIATITAFASGEITYVYVSEALGLGKGTAKLIGWTGFIATAL--- 255
Qy 282 FEPWIKFWRSGAOMPNNIEKNFSRVGTLLVVLIS-----VTILYAGINFSCWSALQLR-LA 335
Db 256 --SYVTSWADYGVKREMYSLLSMLASLSPILLASIKTPTIV-FLGIFLALFSAQSFRPIS 312
Qy 336 DRDLVDKQNGWGMGLHYSVRLVENVMVLFKPGVKVLLNYCHSLIALQLIIAYLISI 395
Db 313 RKVLVAYRRSSLAIG---GLNAVQNVSTFLGGLFGLAYSLGELHSITVNLGLASFLPF 369
Qy 396 DFMLL 400
Db 370 STALI 374
RESULT 4
T02024
cytochrome b245 beta chain homolog rboha - rice (fragment)
N:Alternate names: intrinsic plasma membrane protein RbohaOsp
C:Species: Oryza sativa (rice)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 23-Jul-1999
C:Accession: T02024
R:Keller, T.; Damude, H.G.; Werner, D.; Doerner, P.; Dixon, R.A.; Lamb, C.
submitted to the EMBL Data Library, July 1997
A:Description: A plant homolog of the neutrophil NADPH oxidase gp91phox subunit gene en
A:Reference number: Z14499
A:Accession: T02024
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-745 <REL>
A:Cross-references: EMBL:AF015302; NID:G2654869; PID:G2654870
C:Genetics:
A:Gene: rboha
C:Keywords: calcium binding; membrane protein
Query Match 5.2%; Score 119.5; DB 2; Length 745;
Best Local Similarity 20.7%; Pred. No. 0.047;
Matches 89; Conservative 66; Mismatches 171; Indels 103; Gaps 18;
Qy 40 STPLYC-GEAASALYVIRYKNSYRMTY-TFSPFMPSSIMVQLTLIFVHRDLAKDKP 97
Db 11 SDAECIGTWESKEFALELFDLTLSRRRQMKVDITNKDELREINQOIT-----DNSFDSR 64
Qy 98 LSLFMHLIILGPIRCLEAMIKYL-----TLWKKEQEPEYVSLTRKMKLIDGEEVL 149
Db 65 LQIFFEVDKNDAGRITAEVKEIIMLSASANKLSRLKEQAEEYAAALIMEELDPGLGYI 124

QY 150 IEWEVGHSHIRTLAMHRNAYKRMQSI-----QAFGLGVPQLTYQLYVSLISAEVPLGRWL 204
 Db 125 ELWQ-----LETLLQKQDTMYNSQALSYSQALSQNLAGLRKSSIRKIS----- 170
 QY 205 MVFSLVSVTYGATLCNMLAIOIKYDDYKIRGLPVLVCITI-----WRTLEITSRLIL 258
 Db 171 -----TSLSY-----YFEDNWKRLWL--ALWIGIMAGLFTWKFMQYRNYVFD 212
 QY 259 VL-ESATLKLKAVPFLVLNFIILFE-----PMIKFWRSGAOMPNNIEKNFSRVGTLVV 311
 Db 213 VMGVCVTTAKGAETLKLNMAIILLPCVNRITWLRSTRARALPFDNINFKHTIAAI 272
 QY 312 LISVTILYAGINFSCWALQURLADRLVDKQNGHMLHY-----SVRLAVENIMVLV 366
 Db 273 VVGI-ILHAGNHLVCDPRLIKSDEKAPLQGVFGEIKPTFTLVKGVGEGITGVIMVVC 331
 QY 367 F-----KFEVGVLLNLYCHSL-----IALQLII-----AYLISID 396
 Db 332 MIIAFTLATRWRFRSLVKLPFPDKLTGFNAFW-YSHHLFIIVYIALIVHGECLYLHVV 390
 QY 397 FMLLFFOYL 405
 Db 391 YRRTWML 399

RESULT 5
 A96825
 hypothetical protein T8K14.18 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: A96825
 R:Theologite, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A96825
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-783 <STO>
 A:Cross-references: GB:AE005173; NID:g4835769; PIDN:AAD30236.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T8K14.18
 A:Map position: 1

Query Match 5.1%; Score 118.5; DB 2; Length 783;
 Best Local Similarity 19.6%; Pred. No. 0.06;
 Matches 89; Conservative 69; Mismatches 166; Indels 129; Gaps 19;

QY 73 FFMFSSIMVQLTIFVHRDL-----AKDKPLSLFHLILLGPVIRCLEAMIKYLTWL 124
 Db 16 ENPLNTFIQACILVFSQLFYLKPCQAGPVAQIAGIVLSPVLLSRIPKVEFLQ 75
 QY 125 KKEEQEEPPVS--LTRKQNLIDGEEVLIEWGVHSHIRTLAMHRNAYKRMQSI--QAFLL-- 178
 Db 76 KNAADYSPFSPALRTSPMFLGLEVDLHF-----MRRN-FKAAAVITLSSFFVS 124
 QY 179 GSVQQLTYQLYVSLISAEVPLGRVVLVAFVSLVSYTGATLCNMLAIOIKYDDYKI---RL 235
 Db 125 GLLSFASLMLFIPFLGKEDYFTFPLVLLTSLNTASPVVRSIA-----DWKLTCEI 178
 QY 236 GPVELVCITITWRTLEITSRLILVFSATLKLKAVPFLVLNFIILFE-----PMIKFWR 291
 Db 179 GRLTISCALFELTNVLYTIIIMAFISGIIIELEFLFLATVALLINNVAPWU----- 233
 QY 292 GAQMPNNIEKNFSRVGTLVLI-----SVTILYAGINFSCWALQURLA 335

[illegible]

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-461 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK81229.1; PID:g15026374; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3295

Query Match 4.7%; Score 109.5; DB 2; Length 461;
Best Local Similarity 20.5%; Pred.No. 0.19; Mismatches 91; Conservative 79; Indels 129; Gaps 24;

Qy 33 FPP-SILFSTPLYCGEASALYVMRYIY-RKNSETYR-----MTYTFSPFMF 76
||| :
Db 58 FPIQKILIAMGLLATGAST-YAARVIGEKNYKELKKIVINSCALTIVSIISFIIFQP 116
||| :
Qy 77 -SSIMVOQLTIFVRHDAKOK--PLSL-FMHILLGPVIRCLEAMIKYLTLLWKKEQEPEP 132
||| :
Db 117 KSSLTLYSLG-----ASDNTYPMAVQYISIILFGSIFMCLASVMSYI----- 157
||| :
Qy 133 YVSITRKMLIDGB-----EVLEWEV-----GHSIRTILAMHRNAKYRMSQIOAF 177
||| :
Db 158 MVSUGKTKLTYTNIVGVLLNIINYVVTLQHMGIRGSGIATV-----LSQLAAF 208
||| :
Qy 178 LGSVPQLTY-----QLYVSLISAEPVLRVLMVFSLSVTVYGATLCNMLAFOI 226
||| :
Db 209 VVALQVAYNNKKNQFFENISTNISGGDI-IREIVLVGFSTIIETADAVVSALLNVV 267
||| :
Qy 227 KY-----DDYKIRLGPLEVCITIWR-TLETSRLLLIHLVFS-----ATLKKA 269
||| :
Db 268 LYAGGSDSAIIMLVITKVYMFMEITVIGISSGMOPIVGYNFAGNAGNYKAKDKILKFSLKT 327
||| :
Qy 270 V----PFLVLNFLILPEPIKWFRSQAQPNNEKNFSRGTLVLVISVTILYAGINF 325
||| :
Db 328 VIITSAPFWVGPF-IIWAQPLIGFLPKDALVKSTVSAPRIIVISMPLDG---IYYVAIYY 384
||| :
Qy 326 CWSALQLRLADRLVDXQNGWGHGLHYSVRLVENIAM-----VLVFKFFGVK-VLLNYC 379
||| :
Db 385 -----QAIGEARI SFILSIYRELIMFIPMAVILFKVINGVFIAY- 425
||| :
Qy 380 HSLIALQIIITAYLISIDFMLFPQ 403
||| :
Db 426 ---PLTDIIIVLTYSVYFIRRAFK 445
||| :

RESULT 9
Tl1039
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Chlamydomonas eugametos
C:Species: mitochondrion Chlamydomonas eugametos
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: Tl1039
R:Denovan-Wright, E.M.; Nedelcu, A.M.; Lee, R.W.
Plant Mol. Biol. 36, 285-295, 1998
A>Title: Complete sequence of the mitochondrial DNA of Chlamydomonas eugametos.
A:Reference number: Z17244; MUID:98145434; PMID:9484440
A:Accession: Tl1039
A>Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A:Residues: 1-498 <DEN>
A:Cross-references: EMBL:AF008237; NID:G2865253; PID:G2865257; PIDN:AAC39340.1
C:Genetics:
A:Genome: mitochondrion
A>Note: nad4
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 4.7%; Score 109.5; DB 2; Length 498;
Best Local Similarity 22.1%; Pred.No. 0.2;
Matches 64; Conservative 46; Mismatches 89; Indels 91; Gaps 13;

Qy 185 TYQLYVSLISAEPVLRVLMVFSLSVTVYGA-----TLCNMLAIQIKDYDKIRL- 235
||| :
Db 40 TYCYLFVTVV-----VLLMTYLWISI-YDAIGHSLQMVVIIERLHISFGVDSMSISLT 90
||| :

